

Spacing Between Adjacent Bases
(for Different Number of Peaks Used for Alignment of Raw Data
(M13, Long Gel, 55C, T=6%)

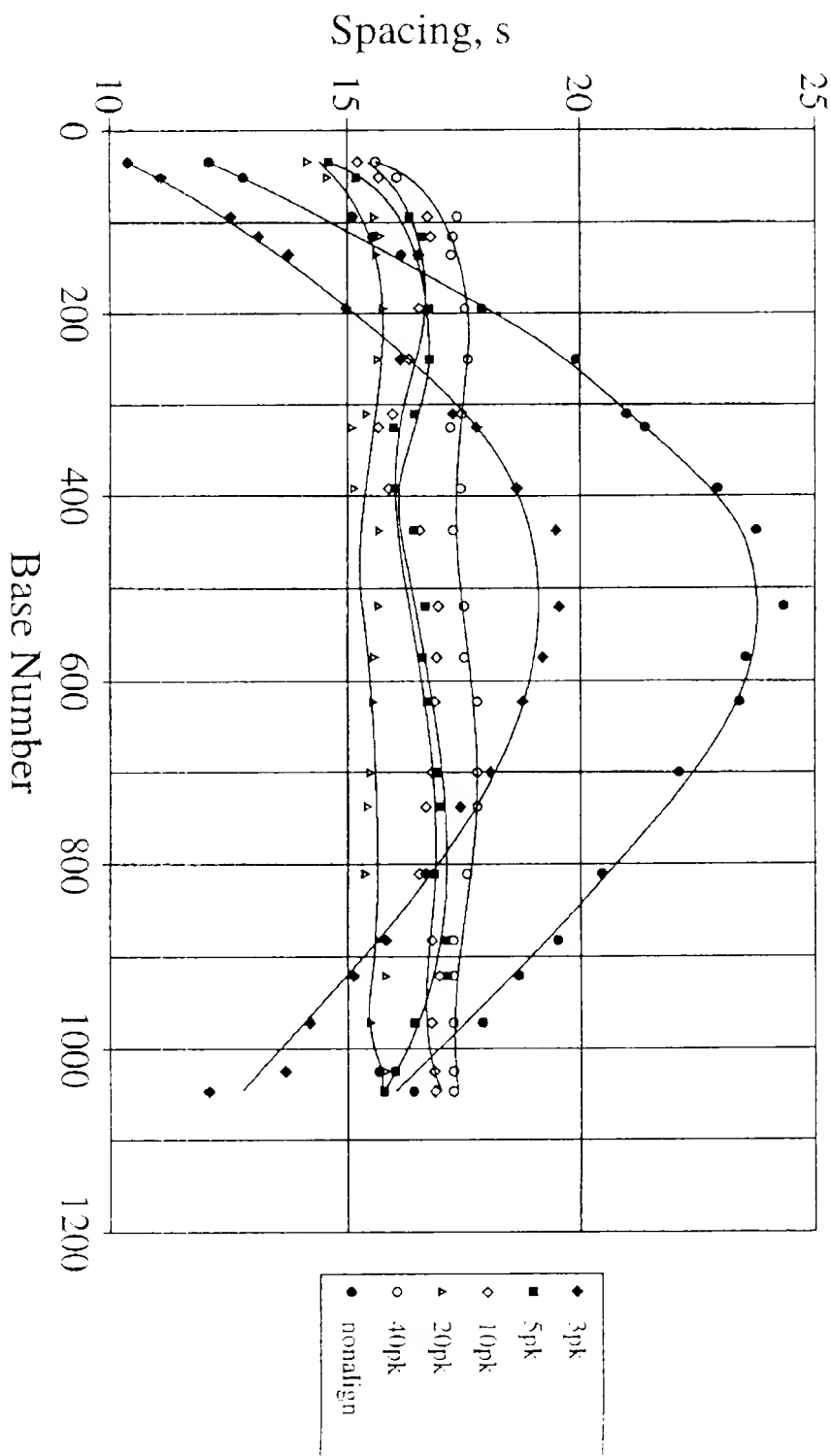


FIG. 2

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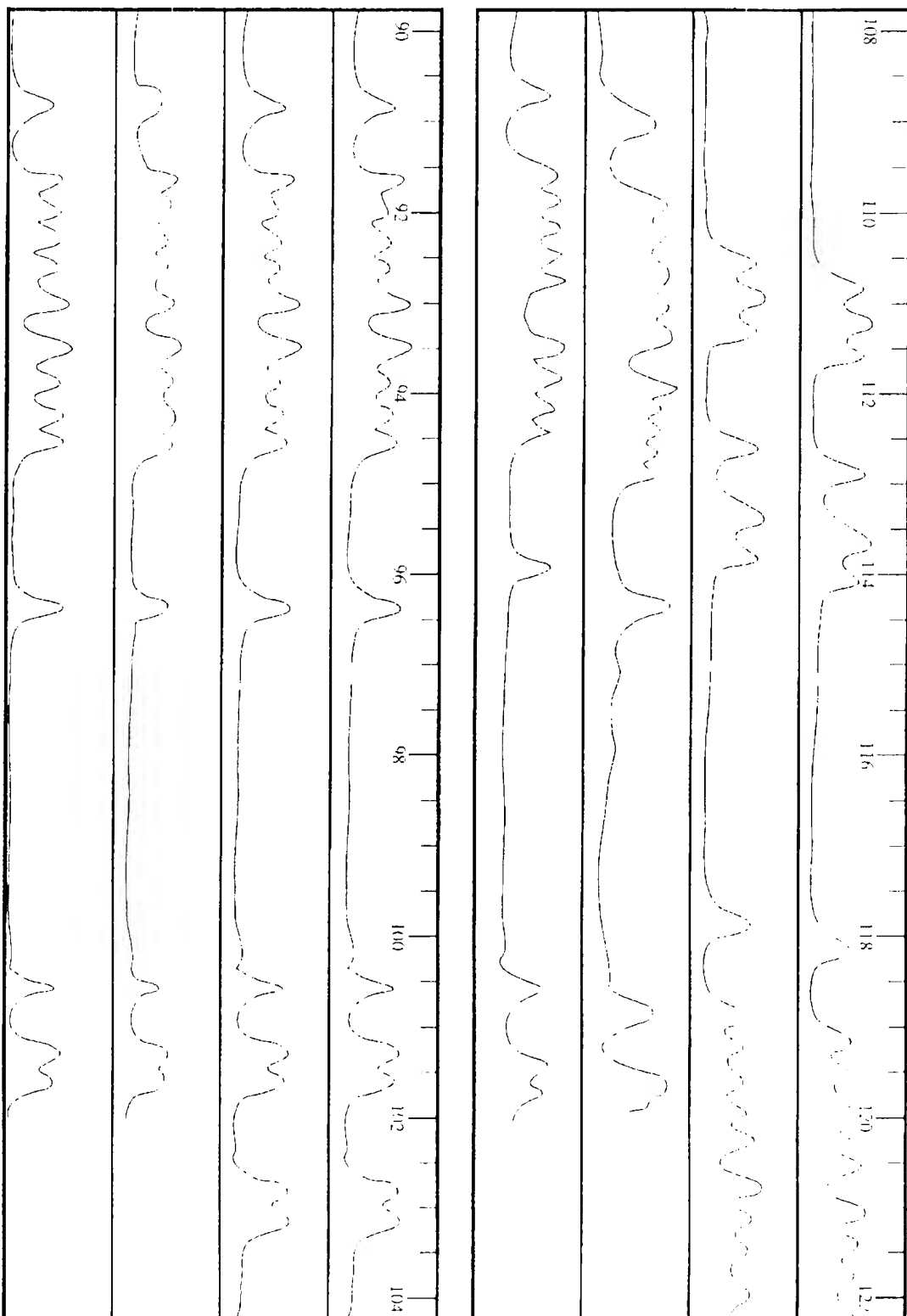


FIG. 4

HIV-1 TruGene Kit (version 0.80)

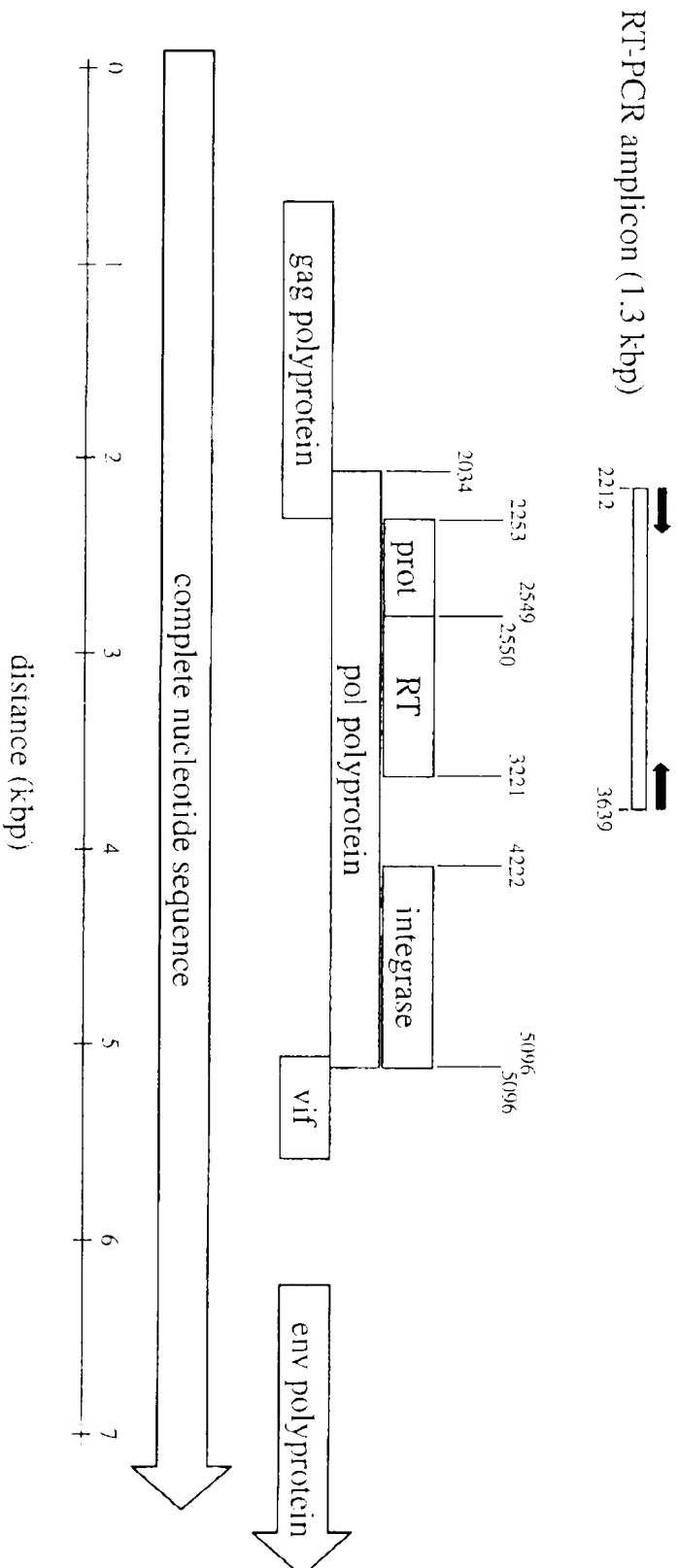


FIG. 6

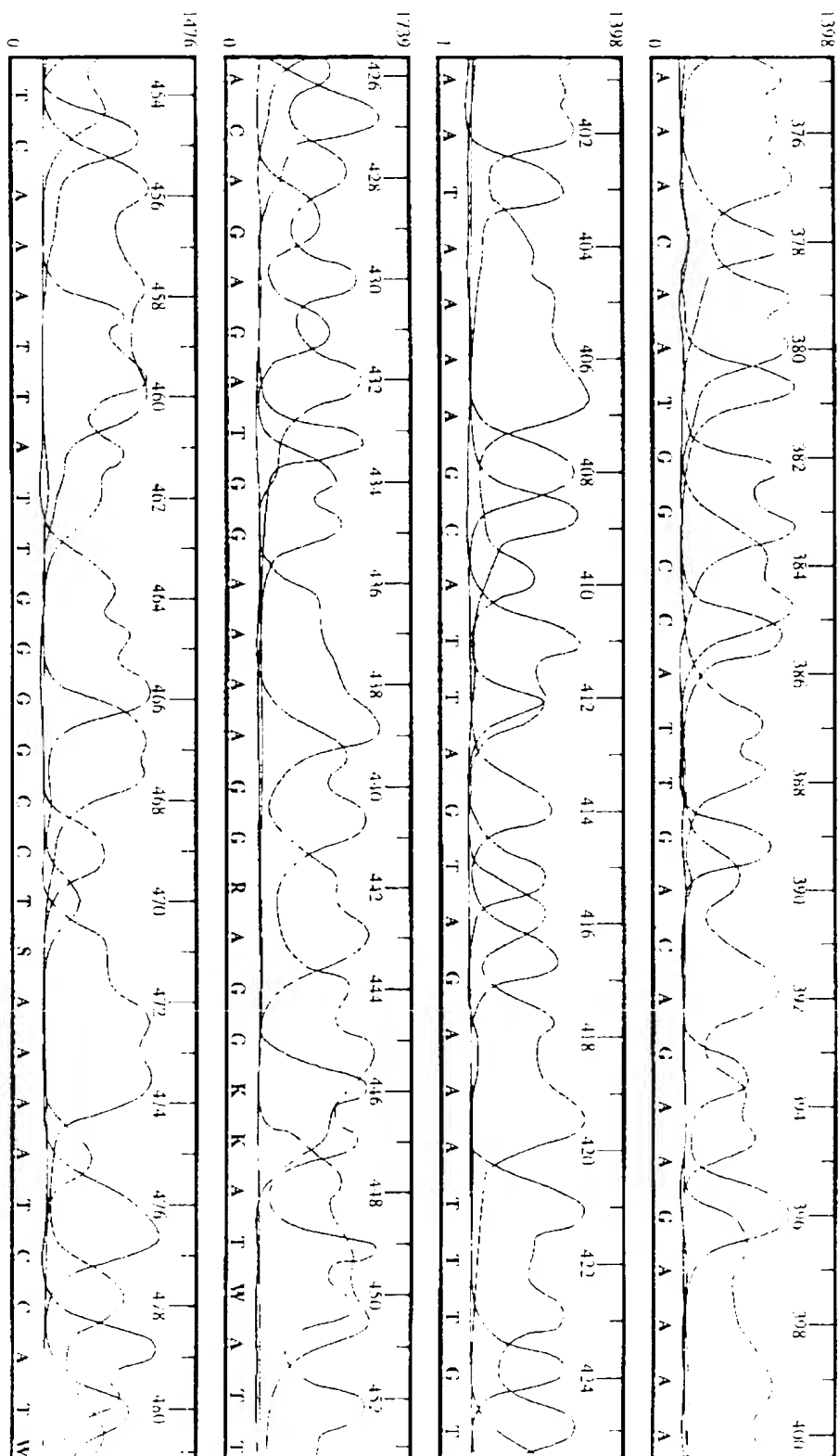


FIG. 7



Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

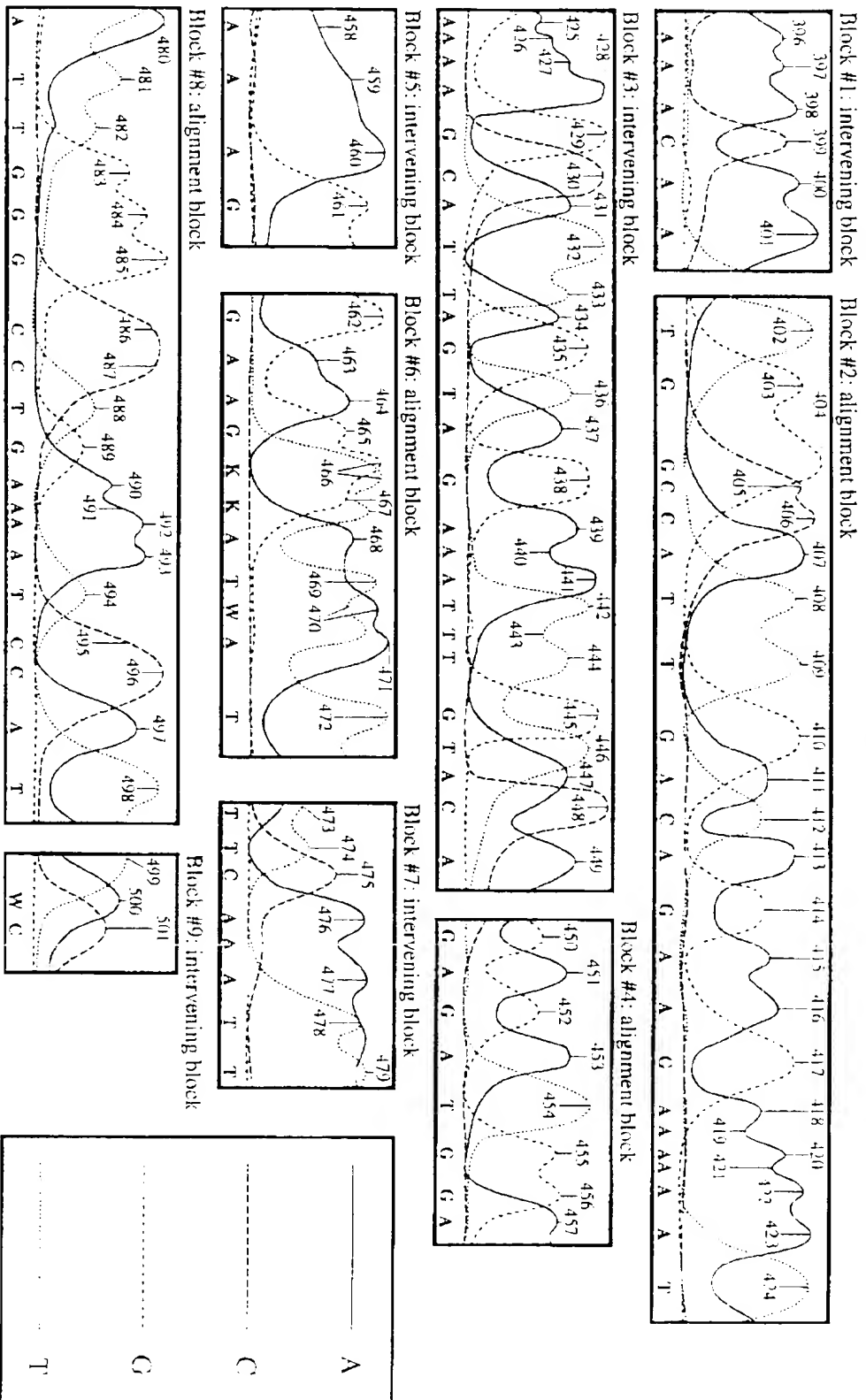


FIG. 8

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Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

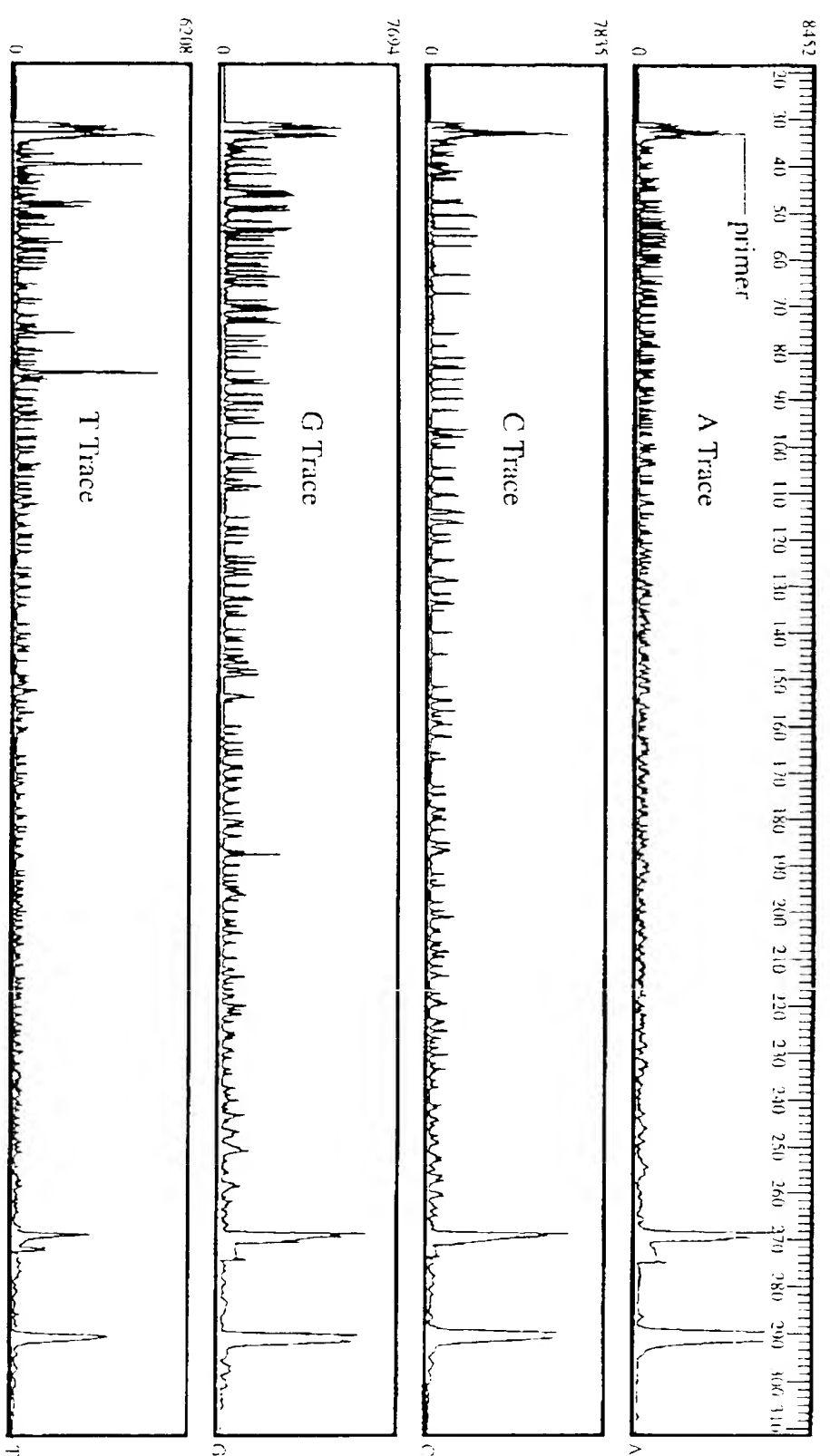


FIG. 9A

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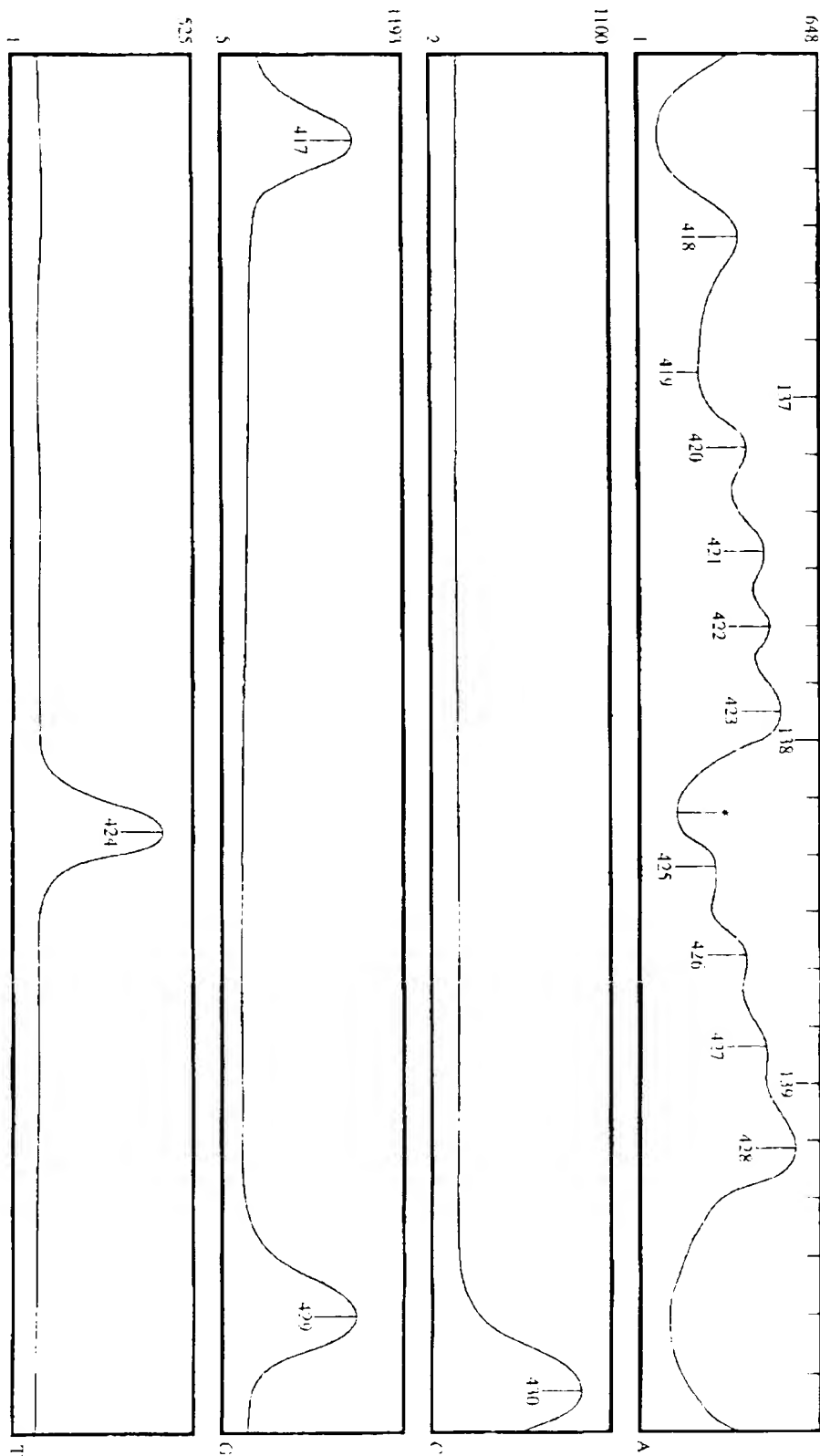


FIG. 9B

Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

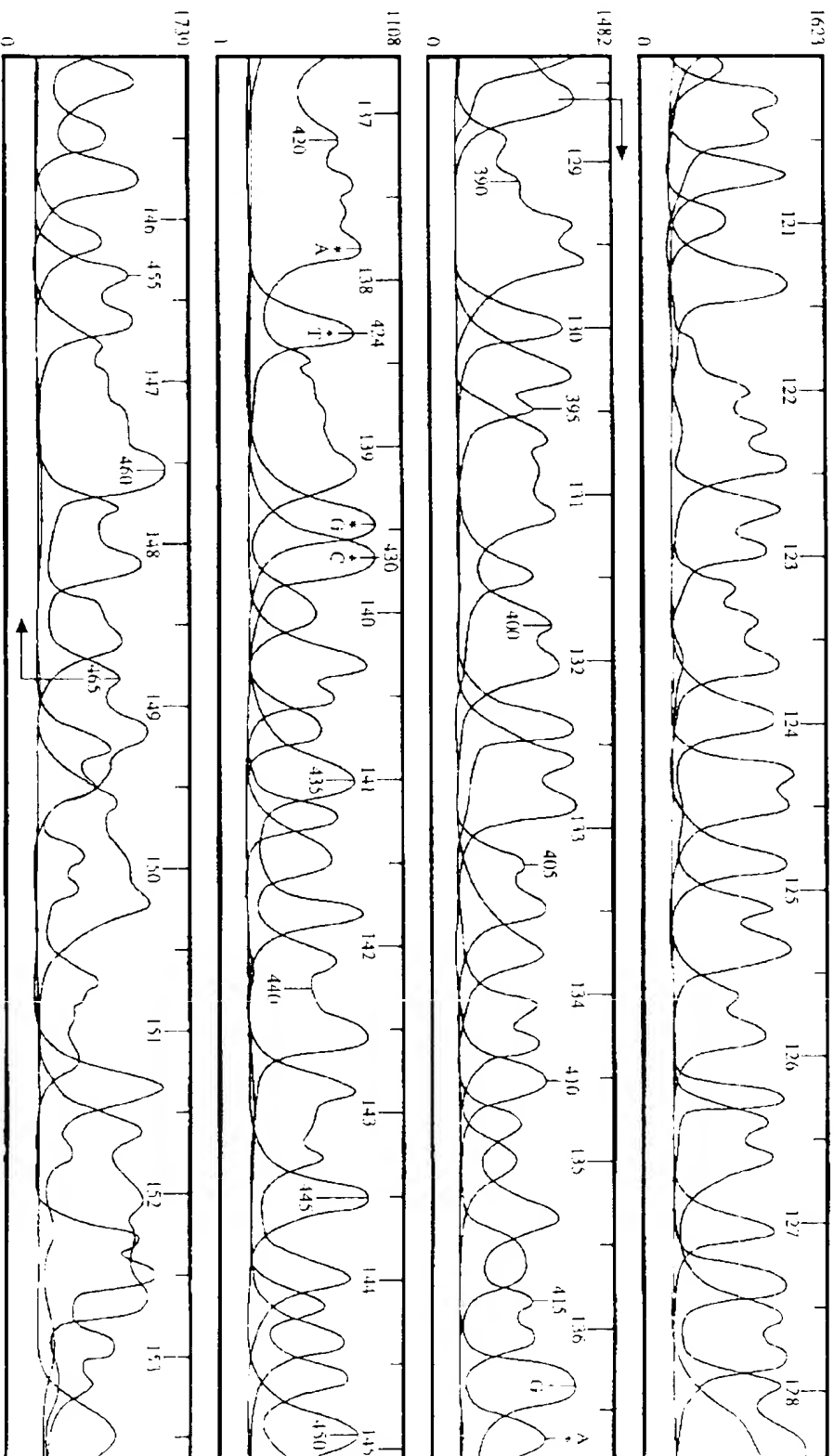
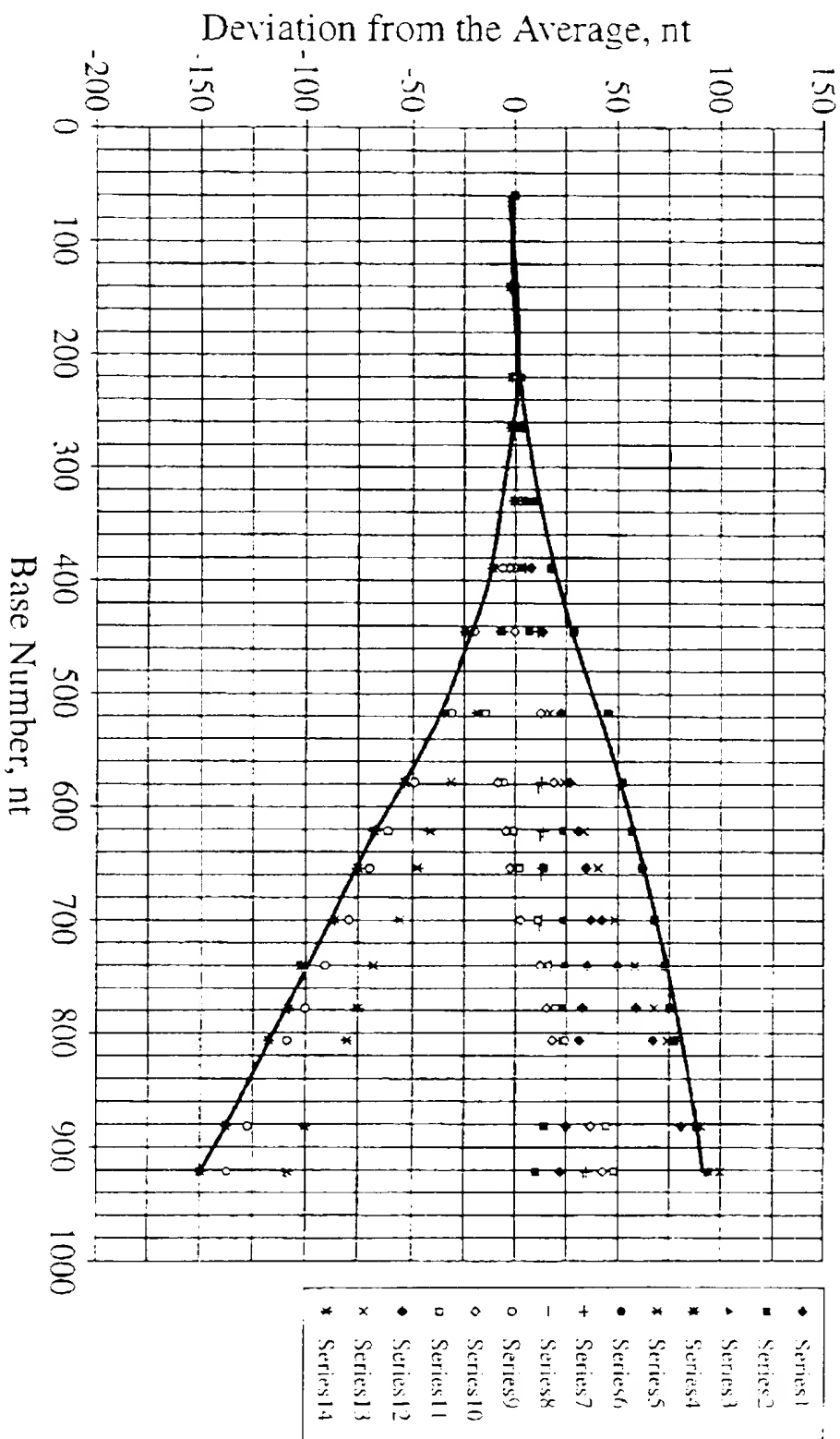


FIG. 9C

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Deviation of the Peak Position (in Number of Bases) from the Average as a Function of Base Number in Different Traces Before Alignment





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Deviation of the Peak Position (in Number of Bases) from the Average
as a Function of Base Number in the Traces Aligned with Internal Standards
(long gel, M13, 17 peaks, 5-th degree polynomial)

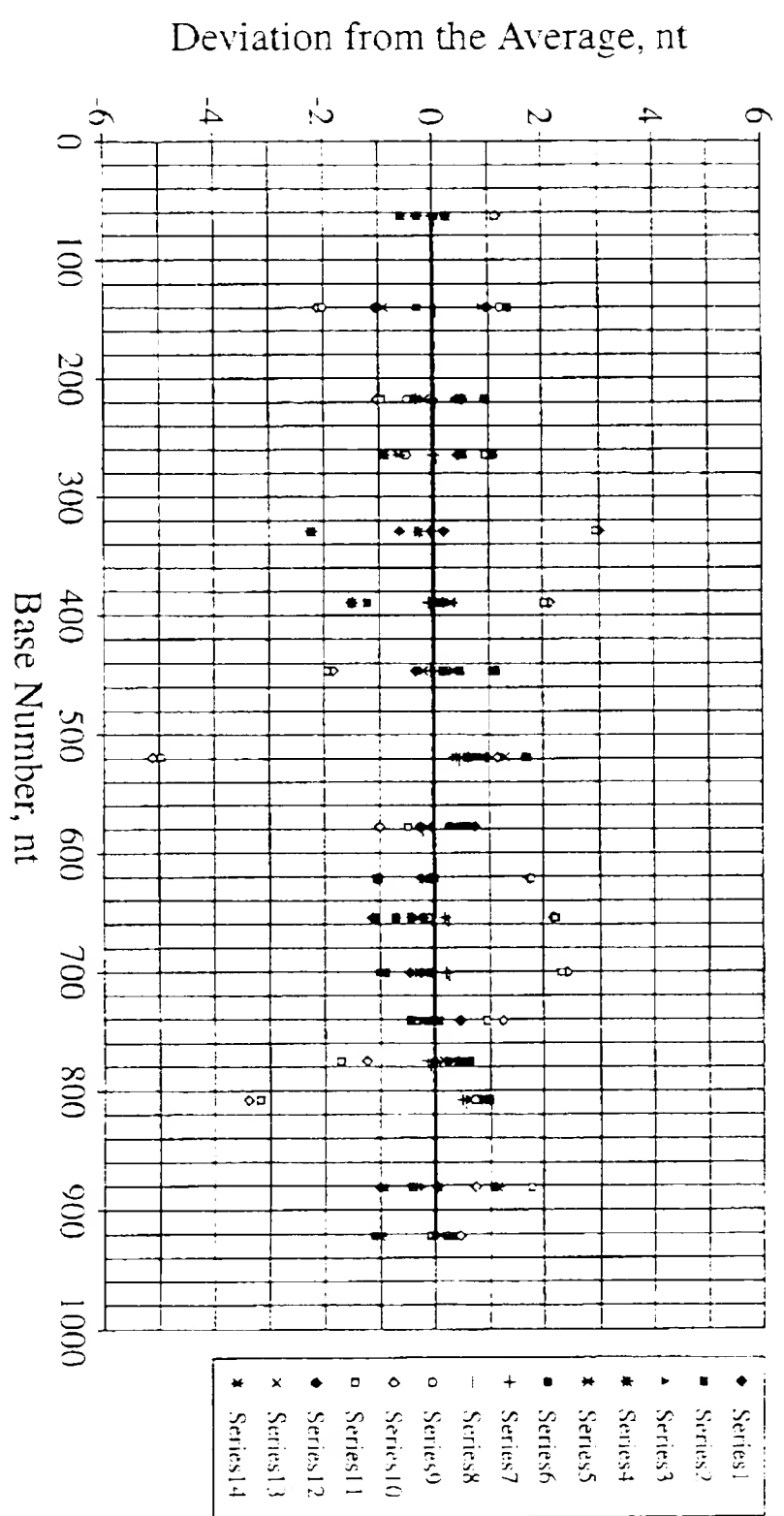


FIG. 11